Amendments to the Specification

Please replace the last paragraph on page 30 (lines 21-27) that continues on page 31 (lines 1-21) with the following amended paragraph:

In order to construct the transgene, the cDNA encoding the mutated human PS1 was subcloned between the SmaI and BamHI restriction sites of the polylinker of the transgenic expression vector HMG (Czech et al., 1997). For microinjecting, the vector sequences were removed by restricting with the enzyme NotI, and the fragment containing the expression cassette was purified by gel electrophoresis. The purified fragment was diluted in 10 mM Tris-HCl (pH 7.4) 0.1 mM EDTA to a final concentration of 2.5 ng/μl and injected into one of the two pronuclei of fertilized mouse embryos. The surviving embryos were immediately transplanted into the oviduct of adoptive (pseudopregnant) mothers. The presence of the transgene in the neonates was determined either by PCR or by performing a Southern analysis. The PCR was carried out using oligomers corresponding to human PS1 (SEQ ID No. 1: 5'-TAA TTG GTC CAT AAA AGG C- 3'; SEQ ID No. 2: 5'-GCA CAG AAA GGG AGT CAC AAG-3'), thereby amplifying a fragment of 550 bp in size. In the case of the Southern blot, a 1.2 kb PstI-SalI fragment from the first intron from the HMG expression cassette, which fragment was radiolabelled with alphaP-32-dCTP, was used as a probe for detecting the transgene and the endogenous HMG gene, as an internal control. Taken overall, these analyses are able to exclude the possibility of there having been any major rearrangement in, or deletions of, the transgene in the founders and their progeny.

Please replace the paragraph on page 34 (lines 1-27) that continues on page 35 (lines 1-3) with the following amended paragraph:

The mutagenesis of the APP was described previously (Czech et al. 1997), and the mutated APP sequences were introduced into the APP_{751} cDNA by inserting the exon-8-containing Sma I/Bgl II APP fragment into the Bluescript vector containing the

mutations. In order to optimize the translation initiation site of the APP, an optimized Kozak consensus sequence was introduced by site-directed mutagenesis carried out by means of PCR. For the PCR, the oligonucleotide combination was as follows: sense oligo (initiation region): SEQ ID No. 3: ccc ggg tcc acc atg ctg ccc ggt ttg g (Kozak sequence underlined), antisense oligo: SEQ ID No. 4: ttc agg gta gac ttc ttg gc. The PCR product was cloned into pCR2 (Invitrogen, France), after which it was sequenced and then subcloned into the APP_{751}SL cDNA-containing Bluescript vector using Sma I and Acc I, thereby deleting the 5' UTR of the APP and introducing the Kozak consensus sequence. In order to generate the transgenic APP_{751} Kozak SL Thy-1 construct, the above APP cDNA, extended in 3' to Cla I (2699) was subcloned into a modified Bluescript vector containing two Sal I sites on each side of the insert. The vector was digested with Sal I and the insert was cloned into the murine Thy-1 vector using the Xho I site (Lüthi et al. J. Neuroscience 17, 4688-4699). The correct orientation was verified by restriction analysis, and the construct was sequenced at the ligation sites. For microinjecting, the cassette was linearized by Not I-Pvu I restriction and the fragment containing the transgene was then purified.